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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/530,209A

DATE: 04/26/2001

TIME: 12:14:59

Input Set : A:\190337.txt

Output Set: N:\CRF3\04262001\I530209A.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Inze, Dirk

6 De Veylder Lieven

7 De Almeida Janice

9 (ii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof

11 (iii) NUMBER OF SEQUENCES: 4

C--> 13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Nixon Peabody LLP

15 (B) STREET: 990 Stewart Avenue

16 (C) CITY: Garden City

17 (D) STATE: New York, New York

C--> 18 (F) ZIP: 11530

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/530,209A

C--> 28 (B) FILING DATE: 13-Jun-2000

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: EP PCT/EP98/06749

33 (B) FILING DATE: 23-OCT-1998

34 (A) APPLICATION NUMBER: EP 97.203.303.9

35 (B) FILING DATE: 24-OCT-1997

38 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

41 (A) LENGTH: 927 base pairs

42 (B) TYPE: nucleic acid

43 (C) STRANDEDNESS: double

44 (D) TOPOLOGY: linear

46 (ii) MOLECULE TYPE: cDNA

48 (iii) HYPOTHETICAL: NO

50 (ix) FEATURE:

51 (A) NAME/KEY: CDS

52 (B) LOCATION: 1..927

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

56	ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC	48
57	Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn	
58	1 5 10 15	
60	GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG	96
61	Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser	
62	20 25 30	
64	ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG	144
65	Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met	

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66	35	40	45	
68	GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC	192		
69	Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile			
70	50 55 60			
72	AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT	240		
73	Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp			
74	65 70 75 80			
76	GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA	288		
77	Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro			
78	85 90 95			
80	TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT	336		
81	Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val			
82	100 105 110			
84	CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG	384		
85	His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val			
86	115 120 125			
88	GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG	432		
89	Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met			
90	130 135 140			
92	TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA	480		
93	Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys			
94	145 150 155 160			
96	TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA	528		
97	Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg			
98	165 170 175			
100	TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG	576		
101	Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys			
102	180 185 190			
104	ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA	624		
105	Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser			
106	195 200 205			
108	TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT	672		
109	Leu Gln Val Ile Ala Ser Thr Lys Gly Ile Asp Phe Leu Glu Phe			
110	210 215 220			
112	AGA CCT TCT GAA GCT GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA	720		
113	Arg Pro Ser Glu Ala Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu			
114	225 230 235 240			
116	TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA	768		
117	Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser			
118	245 250 255			
120	CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT	816		
121	Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser			
122	260 265 270			
124	GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA	864		
125	Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val			
126	275 280 285			
128	TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT	912		
129	Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr			
130	290 295 300			

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132 ACA CAT CTT TCT TAA  
 133 Thr His Leu Ser  
 134 305  
 137 (2) INFORMATION FOR SEQ ID NO: 2:  
 139 (i) SEQUENCE CHARACTERISTICS:  
 140 (A) LENGTH: 308 amino acids  
 141 (B) TYPE: amino acid  
 142 (D) TOPOLOGY: linear  
 144 (ii) MOLECULE TYPE: protein  
 145 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 147 Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn  
 148 1 5 10 15  
 150 Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser  
 151 20 25 30  
 153 Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met  
 154 35 40 45  
 156 Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile  
 157 50 55 60  
 159 Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp  
 160 65 70 75 80  
 162 Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro  
 163 85 90 95  
 165 Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val  
 166 100 105 110  
 168 His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val  
 169 115 120 125  
 171 Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met  
 172 130 135 140  
 174 Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys  
 175 145 150 155 160  
 177 Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg  
 178 165 170 175  
 180 Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys  
 181 180 185 190  
 183 Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser  
 184 195 200 205  
 186 Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe  
 187 210 215 220  
 189 Arg Pro Ser Glu Ala Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu  
 190 225 230 235 240  
 192 Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser  
 193 245 250 255  
 195 Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser  
 196 260 265 270  
 198 Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val  
 199 275 280 285  
 201 Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr  
 202 290 295 300  
 204 Thr His Leu Ser

927

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205 305

208 (2) INFORMATION FOR SEQ ID NO: 3:

210 (i) SEQUENCE CHARACTERISTICS:

211 (A) LENGTH: 25 base pairs

212 (B) TYPE: nucleic acid

213 (C) STRANDEDNESS: single

214 (D) TOPOLOGY: linear

216 (ii) MOLECULE TYPE: other nucleic acid

217 (A) DESCRIPTION: /desc = "oligonucleotide"

219 (iii) HYPOTHETICAL: YES

221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

223 GAACACTCGA GTGTAATGGC AGAGG

25

227 (2) INFORMATION FOR SEQ ID NO: 4:

229 (i) SEQUENCE CHARACTERISTICS:

230 (A) LENGTH: 26 base pairs

231 (B) TYPE: nucleic acid

232 (C) STRANDEDNESS: single

233 (D) TOPOLOGY: linear

235 (ii) MOLECULE TYPE: other nucleic acid

236 (A) DESCRIPTION: /desc = "oligonucleotide"

238 (iii) HYPOTHETICAL: YES

240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

242 CATCATACTA GTTATAATAA TGTAAG

26

## VERIFICATION SUMMARY

DATE: 04/26/2001

PATENT APPLICATION: US/09/530,209A

TIME: 12:14:41

Input Set : A:\190337.txt

Output Set: N:\CRF3\04262001\I530209A.raw

L:13 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]  
L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]